Dynamic changes in the copy number of pluripotency and cell proliferation genes in human ESCs and iPSCs during reprogramming and time in culture.

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Public Summary:
Genomic stability is critical for the clinical use of human embryonic and induced pluripotent stem cells. We performed high-resolution SNP (single-nucleotide polymorphism) analysis on 186 pluripotent and 119 nonpluripotent samples. We report a higher frequency of subchromosomal copy number variations in pluripotent samples compared to nonpluripotent samples, with variations enriched in specific genomic regions. The distribution of these variations differed between hESCs and hiPSCs, characterized by large numbers of duplications found in a few hESC samples and moderate numbers of deletions distributed across many hiPSC samples. For hiPSCs, the reprogramming process was associated with deletions of tumor-suppressor genes, whereas time in culture was associated with duplications of oncogenic genes. We also observed duplications that arose during a differentiation protocol. Our results illustrate the dynamic nature of genomic abnormalities in pluripotent stem cells and the need for frequent genomic monitoring to assure phenotypic stability and clinical safety

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